## SEQUENCE LISTING

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(1) GENERAL INFORMATION:

(i) APPLICANT: Crabtree, Gerald R.
Schreiber, Stuart L.
Spencer, David M.
Wandless, Thomas J.
Belshaw, Peter

(ii) TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED GENES AND OTHER BIOLOGICAL EVENTS

(iii) NUMBER OF SEQUENCES: 81

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP

(B) STREET: One Post Office Square

(C) CITY: Boston

(D) STATE: MA

(E) COUNTRY: USA

(F) ZIP: 02109-2170

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: APV-316.15

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	_	
(2) IN	FORMATION SEQ ID NO:1:	
΄(:	<ul> <li>i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 14 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>	
(i.	i) MOLECULE TYPE: peptide	
(x.	i) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
Met Gl	y Ser Ser Lys Pro Lys Asp Pro Ser Gln Arg 5 10	
(2) IN	FORMATION FOR SEQ ID NO:2:	
(.	i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 11 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(i	i) MOLECULE TYPE: cDNA	
(x.	i) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
GTTAAG	TTAA C	11
(2) IN	FORMATION FOR SEQ ID NO:3:	
(	i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 11 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
· (i	i) MOLECULE TYPE: cDNA	
(x	i) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
TGACTC	AGCG C	11
(2) IN	FORMATION FOR SEQ ID NO:4:	
(	<ul> <li>i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 33 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>	

- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION: 6..11
  - (D) OTHER INFORMATION: /note= "Sac II restriction site."
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_signal
  - (B) LOCATION:  $12..\overline{16}$
  - (D) OTHER INFORMATION: /note= "Kozak sequence."
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 17..31
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 17..33
  - (D) OTHER INFORMATION: /note= "Region of homology with target sequence."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGACACCGCG GCCACC ATG GCC ACA ATT GGA GC
Met Ala Thr Ile Gly
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Thr Ile Gly
1 5

- (2) INFORMATION FOR SEQ ID NO. 6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 27 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

- (ix) FEATUR
  - (A) NAME/KEY: misc feature
  - (B) LOCATION: 6..11
  - (D) OTHER INFORMATION: /note= "Xho I restriction site."
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION:  $12..\overline{27}$
  - (D) OTHER INFORMATION: /note= "Region of homology with target sequence."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6: CGACACTCGA GAGCCCATGA CTTCTGG
- (2) INFORMATION FOR SEQ ID NO:7:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 1..4
    - (D) OTHER INFORMATION: /note= "Translation product of complement of SEQ ID NO:6, bases 9 to 20."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Trp Ala Leu

- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 41 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION: 6..11

- A INFORMATION: /note= "Xho striction site." (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 12..41 (D) OTHER INFORMATION: /note= "Region of homology with target sequence." (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 9..41 (ix) FEATURE: (A) NAME/KEY: misc\_feature (B) LOCATION: 28 (D) OTHER INFORMATION: /note= "A to G." (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: CGACACTC GAG CTC TGC TAC TTG CTA GGT GGA ATC CTC TTC 41 Glu Leu Cys Tyr Leu Leu Gly Gly Ile Leu Phe 1 (2) INFORMATION FOR SEQ ID NO:9: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: Glu Leu Cys Tyr Leu Leu Gly Gly Ile Leu Phe 5 (2) INFORMATION FOR SEQ ID NO:10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA
- - (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 3..8
- (D) OTHER INFORMATION: /note= "Eco RI restriction site."

(ix) FEATUR (A) NAME/KEY: misc feature

(B) LOCATION: 9..24

(D) OTHER INFORMATION: /note= "Region of homology with target sequence."

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 24

(D) OTHER INFORMATION: /note= "G to C."

## (ix) FEATURE:

(A) NAME/KEY: misc\_signal

(B) LOCATION: complement (9..11)

(D) OTHER INFORMATION: /note= "Translational stop encoded in complementary strand."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGAATTCTT AGCGAGGGGC CAGC

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..4

(D) OTHER INFORMATION: /note= "Translational product of complement to SEQ ID NO:10, bases 12 to 23."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Ala Pro Arg

1

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 3..8
  - (D) OTHER INFORMATION: /note= "Eco RI restriction."
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION: 12..17
  - (D) OTHER INFORMATION: /note= "Sal I restriction site."
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_signal
  - (B) LOCATION: complement (9..11)
  - (D) OTHER INFORMATION: /note= "Translational stop signal encoded on complementary strand."
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION: 18..33
- (D) OTHER INFORMATION: /note= "Region of homology with target sequence."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGAATTCTT AGTCGACGCG AGGGGCCAGG GTC

33

- (2) INFORMATION FOR SEQ ID NO:13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 1..4
    - (D) OTHER INFORMATION: /note= "Translational product of complement to SEQ ID NO:12, bases 18 to 29."
  - (xi) SEQUENCE DESCRIPTION ₹ SEQ ID NO:13:

Leu Ala Pro Arg

- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 base pairs

25

- .ucleic acid (B) TY (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 4..9
  - (D) OTHER INFORMATION: /note= "Xho I restriction site."
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 13
  - (D) OTHER INFORMATION: /note= "T to G."
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION:  $4..2\overline{5}$
  - (D) OTHER INFORMATION: /note= "Region of homology with target sequence."
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 10..24
- (xi) SEQUENCE DESCRIPTION: SEQ. ID NO:14:

GGGCTCGAG CTC GGC TAC TTG CTA G Leu Gly Tyr Leu Leu

- (2) INFORMATION FOR SEQ ID NO:15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Gly Tyr Leu Leu 1

- (2) INFORMATION FOR SEQ ID NO:16:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 26 base pairs
    - (B) TYPE: nucleic acid

- (C) S NJEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: misc\_feature (B) LOCATION:  $6..1\overline{1}$ (D) OTHER INFORMATION: /note= "Xho I restriction site." (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION:  $12..\overline{2}6$ (D) OTHER INFORMATION: /note= "Region of homology with target sequence." (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16: CGACACTCGA GGTGACGGAC AAGGTC \_\_\_\_\_ (2) INFORMATION FOR SEQ ID NO:17: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: misc\_feature (B) LOCATION: 6..11 (D) OTHER INFORMATION: /note= "Sal I restriction site."

  - (ix) FEATURE:
     (A) NAME/KEY: misc feature
    - (B) LOCATION: 12...26
  - (D) OTHER INFORMATION: /note= "Region of homology with target sequence."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

26

- (D) TO wiY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION: 1..5
  - (D) OTHER INFORMATION: /note= "Xho I restriction site."
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 10..15
  - (D) OTHER INFORMATION: /note= "Bsi WI restriction site."
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 6..32
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCGAG TAT CCG TAC GAC GTA CCA GAC TAC GCA G
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1

33

- (2) INFORMATION FOR SEQ ID NO:19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala 1 5

- (2) INFORMATION FOR SEQ ID NO:20:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 33 base pairs
    - (B) TYPE: nucleic adid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION: 1..5

•	(b) Of a INFORMATION: / Hotel Sales Selection		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:		
TCGA	ACTGCGT AGTCTGGTAC GTCGTACGGA TAC	33	
(2)	INFORMATION FOR SEQ ID NO:21:		
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 33 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>		
	(ii) MOLECULE TYPE: cDNA		
	<pre>(ix) FEATURE:     (A) NAME/KEY: misc_feature     (B) LOCATION: 15     (D) OTHER INFORMATION: /note= "Sal I restriction site."</pre>		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:		
TCG	ACTATCC GTACGACGTA CCAGACTACG CAC	33	
(2)	(2) INFORMATION FOR SEQ ID NO:22:		
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 33 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>		
	(ii) MOLECULE TYPE: cDNA		
	<pre>(ix) FEATURE:     (A) NAME/KEY: misc_feature     (B) LOCATION: 15     (D) OTHER INFORMATION: /note= "Xho I restriction site."</pre>		
	(xi) SEQUENCE DESCRIPTION SEQ ID NO:22:	22	
TCG	AGTGCGT AGTCTGGTAC GTCGTACGGA TAG	33	
(2)	INFORMATION FOR SEQ ID NO:23:		
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 80 base pairs		

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: misc\_feature (B) LOCATION:  $6..1\overline{1}$ (D) OTHER INFORMATION: /note= "Sac II restriction site." (ix) FEATURE: (A) NAME/KEY: misc signal (B) LOCATION: 12..16 (D) OTHER INFORMATION: /note= "Kozak sequence." (ix) FEATURE: (A) NAME/KEY: misc\_signal (B) LOCATION:  $17..\overline{5}8$ (D) OTHER INFORMATION: /note= "Myristoylation signal." (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 59..64 (D) OTHER INFORMATION: /note= "Xho I restriction site." (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 65..80 (D) OTHER INFORMATION: /note= "Zeta homology." (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 17..79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23: CGACACCGCG GCCACC ATG GGG AGT AGC AAG AGC AAG CCT AAG GAC CCC 49 Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro 80 AGC CAG CGC CTC GAG AGG AGT GCA GAG ACT G Ser Gln Arg Leu Glu Arg Ser Ala Glu Thr (2) INFORMATION FOR SEQ ID NO:24: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear

nucleic acid

(C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg Leu Glu

Arg Ser Ala Glu Thr 20

- (2) INFORMATION FOR SEQ ID NO:25:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 27 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 12..26
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION: 6..11
    - (D) OTHER INFORMATION: /note= "Xho I restriction site."
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION:  $12..\overline{27}$
  - (D) OTHER INFORMATION: /note= "Region of homology with target sequence."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGACACTCGA G GAG CTC TGT GAC GAT G Glu Leu Cys Asp Asp

(2) INFORMATION FOR SEQ ID NO 26:

- - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein

Glu Léu Cys Asp Asp 1 5

- (2) INFORMATION FOR SEQ ID NO:27:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 41 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION: 6..11
    - (D) OTHER INFORMATION: /note= "Xho I restriction site."
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION: 12..41
    - (D) OTHER INFORMATION: /note= "Region of homology with target sequence."
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION: 27..29
    - (D) OTHER INFORMATION: /note= "GAT to AAG."
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 9..41
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGACACTC GAG CTC TGC TAC TTG CTA AAG GGA ATC CTC TTC Glu Leu Cys Tyr Leu Leu Lys Gly Ile Leu Phe 1 5

- (2) INFORMATION FOR SEQ ID NO; 28:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 11 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

- (2) INFORMATION FOR SEQ ID NO:29:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 44 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION: 6..11
    - (D) OTHER INFORMATION: /note= "Xho I restriction site."
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 9..44
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION:  $27..\overline{4}4$
    - (D) OTHER INFORMATION: /note= "Region of homology with target sequence."

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGACACTC GAG CTG CTG GAT CCG AAG CTC TGC TAC TTG CTA AAG Glu Leu Leu Asp Pro Lys Leu Cys Tyr Leu Leu Lys 1

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Glu Leu Leu Asp Pro Lys Leu Cys Tyr Leu Leu Lys

- (2) INFORMATION FOR SEQ ID NO:31:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LEIGHT: 31 base pairs
  (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 6..11
  - (D) OTHER INFORMATION: /note= "Xho I restriction site."
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 12..31
  - (D) OTHER INFORMATION: /note= "Region of homology with target sequence."
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 9..31
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGACACTC GAG ACA ACA GAG TAC CAG GTA GC
Glu Thr Thr Glu Tyr Gln Val Ala
1 5

31

- (2) INFORMATION FOR SEQ ID NO:32:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 8 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu Thr Thr Glu Tyr Gln Val Ala
1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECUL .PE: cDNA (ix) FEATURE: (A) NAME/KEY: misc\_feature (B) LOCATION: 6..11 (D) OTHER INFORMATION: /note= "Xho I restriction site." (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 12..28 (D) OTHER INFORMATION: /note= "Region of homology with target sequence." (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 9..28 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33: CGACACTC GAG GGC GTG CAG GTG GAG AC Glu Gly Val Gln Val Glu Thr 5 1 (2) INFORMATION FOR SEQ ID NO:34: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34: Glu Gly Val Gln Val Glu Thr 5 (2) INFORMATION FOR SEQ ID NO:35: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(D) OTHER INFORMATION: /note= "Sal I restriction site."

1

(ii) MOLECULE TYPE: cDNA

(A) NAME/KEY: misc feature

(B) LOCATION:  $6..1\overline{1}$ 

(ix) FEATURE:

(ix) FEATURE (A) NAME/KEY: misc\_feature (B) LOCATION: 12..27 (D) OTHER INFORMATION: /note= "Region of homology with target sequence." (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: complement (9..26) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35: CGACAGTCGA CTTCCAGTTT TAGAAGC (2) INFORMATION FOR SEQ ID NO:36: (i) SEQUENCE CHARACTERISTICS: . (A) LENGTH: 6 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36: Leu Leu Lys Leu Glu Val 5 1 (2) INFORMATION FOR SEQ ID NO:37: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION:  $7...\sqrt{2}$
  - (D) OTHER INFORMATION: /note= "Xho I restriction site."
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 10..27
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 13..27

- (D) OTHE INFORMATION: /note= "Regi \_ homology with target sequence."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCGACACTC GAG ACG GGG GCC GAG GGC
Glu Thr Gly Ala Glu Gly
1 5

27

- (2) INFORMATION FOR SEQ ID NO:38:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 6 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) .SEQUENCE DESCRIPTION: SEQ ID NO:38:

Glu Thr Gly Ala Glu Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:39:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 28 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION: 7..12
    - (D) OTHER INFORMATION: /note= "Sal I restriction site."
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: complement (10..18)
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION: 13..28
    - (D) OTHER INFORMATION: /note= "Region of homology with target sequence."

CCGACAGTCG ACCTCTATTT TGAGCAGC	28
(2) INFORMATION FOR SEQ ID NO:40:	. •
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 3 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
Ile Glu Val 1	
(2) INFORMATION FOR SEQ ID NO:41:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 38 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
CGACACCGCG GCCACCATGA AGCTACTGTC TTCTATCG	38
(2) INFORMATION FOR SEQ ID NO:42:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 28 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
CGACAGTCGA CCGATACAGT CAACTGTC	28
(2) INFORMATION FOR SEQ ID NO:43:	-

ESCRIPTION: SEQ ID NO:39:

(xi) SEQUENC

- hARACTERISTICS: (i) SEQUENCE (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE: (A) NAME/KEY: misc feature
  - (B) LOCATION:  $6..1\overline{1}$
  - (D) OTHER INFORMATION: /note= "Sac II restriction site."
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_signal
    - (B) LOCATION: 12..16
    - (D) OTHER INFORMATION: /note= "Kozak sequence."
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 17..37
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION:  $17..\overline{3}8$
  - (D) OTHER INFORMATION: /note= "Gal4 (1-147) coding region."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGACACCGCG GCCACC ATG AAG CTA CTG TCT TCT ATC G Met Lys Leu Leu Ser Ser Ile 1

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - '(B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Lys Leu Leu Ser Ser Ile 5

- (2) INFORMATION FOR SEQ ID NO:45:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 28 base pairs
    - (B) TYPE: nucleic acid

- (C) STR. DNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION: 1..17
  - (D) OTHER INFORMATION: /note= "Region encoding for C-terminal end of Gal4 (1-147)."
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 3..17
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (B) LOCATION:  $18..\overline{23}$
  - (D) OTHER INFORMATION: /note= "Sal I restriction site."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
- GA CAG TTG ACT GTA TCG GTCGACTGTC G Arg Gln Leu Thr Val Ser 1 5

28

- (2) INFORMATION FOR SEQ ID NO:46:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 6 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Arg Gln Leu Thr Val Ser

- (2) INFORMATION FOR SEQ ID NO. 47:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 34 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

LSCRIPTION: SEQ ID NO:47: (xi) SEQUENCE

## CGACACCGCG GCCACCATGG TTTCTAAGCT GAGC

- (2) INFORMATION FOR SEQ ID NO:48:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 28 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: 'linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGACAGTCGA CCAACTTGTG CCGGAAGG

- (2) INFORMATION FOR SEQ ID NO:49:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 34 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION:  $6..1\overline{1}$
    - (D) OTHER INFORMATION: /note= "Sac II restriction site."
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_signal
    - (B) LOCATION:  $12..\overline{16}$
    - (D) OTHER INFORMATION: /note= "Kozak sequence."
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 17..34
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION:  $17..\overline{34}$
    - (D) OTHER INFORMATION: /note= "Region encoding N-terminal end of HNF1 (1281)."

(xi) SEQUENCE SCRIPTION: SEQ ID NO:49:

CGACACCGCG GCCACC ATG GTT TCT AAG CTG AGC Met Val Ser Lys Leu Ser

- (2) INFORMATION FOR SEQ ID NO:50:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 6 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Val Ser Lys Leu Ser . 5

- (2) INFORMATION FOR SEQ ID NO:51:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 28 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION: 1..20
    - (D) OTHER INFORMATION: /note= "Region encoding for C-terminal end of HNF1 (1-282)."
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS (B) LOCATION: 3..17
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CC TTC CGG CAC AAG TTG GTCGAQTGTC G Ala Phe Arg His Lys Leu 1

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6 amino acids

- E: amino acid (B) (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ala Phe Arg His Lys Leu 1

- (2) INFORMATION FOR SEQ ID NO:53:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 11 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: both
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_signal
    - (B) LOCATION: 3..7
    - (D) OTHER INFORMATION: /note= "Kozak sequence."
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION: 1..11
    - (D) OTHER INFORMATION: /note= "Complementary to bases 5 to 15 of SEQ ID NO:54."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCCACCATG C

- (2) INFORMATION FOR SEQ ID NO:54:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 3 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: &ingle
    - (D) TOPOLOGY: linear
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 1..3
    - (D) OTHER INFORMATION: /note= "Translation product of SEQ ID NO:53 and SEQ ID NO:55. Translational start site at base 8 of SEQ ID NO:53."

(2) INFORMATION FOR SEQ ID NO:55: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 14..17 (D) OTHER INFORMATION: /note= "Sac II restriction site overhang." (ix) FEATURE: (A) NAME/KEY: misc\_feature (B) LOCATION: 1..5 (D) OTHER INFORMATION: /note= "Xho I restriction site overhang." (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 5..15 (D) OTHER INFORMATION: /note= "Complementary to bases 1 to 11 of SEQ ID NO:53." (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55: 17 TCGAGCATGG TGGCCGC (2) INFORMATION FOR SEQ ID NO:56: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56: 27 TCGACCCTAA GAMGAAGAGA AAGGTAC (2) INFORMATION FOR SEQ ID NO:57:

(xi) SEQUENCE SCRIPTION: SEQ ID NO:54:

Met Leu Glu

(A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57: 27 TCGAGTACCT TTCTCTTCKT CTTAGGG (2) INFORMATION FOR SEQ ID NO:58: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 1..5 (D) OTHER INFORMATION: /note= "Sal I restriction site overhang." (ix) FEATURE: (A) NAME/KEY: misc\_feature (B) LOCATION: 5..27 (D) OTHER INFORMATION: /note= "Complementary to SEQ ID NO:60, bases 5 to 27." (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58: 27 TCGACCCTAA GAAGAAGAGA AAGGTAC (2) INFORMATION FOR SEQ ID NO:59: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: Peptide (B) LOCATION: 1..11 (D) OTHER INFORMATION: /note= "Translation product of SEQ ID

ARACTERISTICS:

(i) SEQUENCE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59: Leu Asp Pro Lys Lys Lys Arg Lys Val Leu Glu (2) INFORMATION FOR SEQ ID NO:60: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 1..5 (D) OTHER INFORMATION: /note= "Xho I restriction site overhang." (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 5..27 (D) OTHER INFORMATION: /note= "Complementary to SEQ ID NO:58, bases 5 to 27." (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60: 27 TCGAGTACCT TTCTCTTCTT CTTAGGG (2) INFORMATION FOR SEQ ID NO:61: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGACAGTCGA CGCCCCCCG ACCGATGTC

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: 26 CGACACTCGA GCCCACCGTA CTCGTC (2) INFORMATION FOR SEQ ID NO:63: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 6..11 (D) OTHER INFORMATION: /note= "Sal I restriction site." (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 12..29 (ix) FEATURE: (A) NAME/KEY: misc feature (B) LOCATION: 12..29 (D) OTHER INFORMATION: /note= "Region encoding Nterminal end of VP16 (413490)." (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63: 29 CGACAGTCGA C GCC CCC CCG ACC GAT GTC Ala Pro Pro Thr Asp Val (2) INFORMATION FOR SEQ ID NO:64: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein

ARACTERISTICS:

Ala Pro Pro Thr Asp Val

- (2) INFORMATION FOR SEQ ID NO:65:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 26 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..15
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION:  $1..1\overline{5}$
    - (D) OTHER INFORMATION: /note= "Region encoding C-terminal end of VP16 (413-490)."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GAC GAG TAC GGT GGG CTCGAGTGTC G
Asp Glu Tyr Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Asp Glu Tyr Gly Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:67:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 23 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

•	(D) POLOGY: linear	
•	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
GGAATTO	CCAT ATGGGCGTGC AGG	23
(2) INF	FORMATION FOR SEQ ID NO:68:	
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 5 amino acids</li><li>(B) TYPE: amino acid</li><li>(D) TOPOLOGY: linear</li></ul>	
	(ii) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
His Met	Gly Val Gln 5	
(2) INF	FORMATION FOR SEQ ID NO:69:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 39 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
CTGTCCC	GGG ANNNNNNNN TTTCTTTCCA TCTTCAAGC	39
(2) INF	ORMATION FOR SEQ ID NO:70:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 11 amino acids  (B) TYPE: amino acid  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
Arg Ser	Xaa Xaa Xaa Lys Lys Gly Asp Glu Leu 5 10	

## (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 64 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTGTCCCGGG AGGAATCAAA TTTCTTTCCA TCTTCAAGCA TNNNNNNNNN GTGCACCACG 60 CAGG

- (2) INFORMATION FOR SEQ ID NO:72:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Arg Ser Ser Asp Phe Lys Lys Gly Asp Glu Leu Met Xaa Xaa Xaa His 1 5 10 15

Val Val Cys

- (2) INFORMATION FOR SEQ ID NO:73:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 57 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CGCGGATCCT CATTCCAGTT TTAGAAGCTC CACATCNNNN NNNNAGTGG CATGTGG

- (2) INFORMATION FOR SEQ ID NO:74:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acids
    - (B) TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74: . Glu Leu Lys Leu Leu Glu Val Asp Xaa Xaa Xaa Thr Ala His Pro 10 (2) INFORMATION FOR SEQ ID NO:75: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75: CGCGGATCCT CATTCCAGTT TTAGAAGC 28 (2) INFORMATION FOR SEQ ID NO:76: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 5 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76: Glu Leu Lys Leu Leu 1 (2) INFORMATION FOR SEQ ID NO:77: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28\base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii)MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77: 28 CGACAGTCGA CCGATACAGT CAACTGTC

POLOGY: linear

(ii) MOLECULE TYPE: peptide

(D)

(2) INFO	RMATION FOR SEQ ID NO:78:	
•	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 28 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
(	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:	
CGACAGTCG	SA CCAACTTGTG CCGGAAGG	28
(2) INFOR	MATION FOR SEQ ID NO:79:	
	<ul> <li>i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 17 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>	
. (	ii) MOLECULE TYPE: cDNA	
(	xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	
TCGAGCATG	G TGGCCGC	17
(2) INFOR	MATION FOR SEQ ID NO:80:	
(	<ul> <li>i) SEQUENCE CHARACTERISTICS:         <ul> <li>(A) LENGTH: 27 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul> </li> </ul>	
(;	ii) MOLECULE TYPE: cDNA	
. (:	xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
TCGAGTACC	T TTCTCTTCTT CTTAGGG	27
(2) INFOR	MATION FOR SEQ ID NO:81:	
	i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 26 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(i) MOIFCHIF TYPE: COND	

CGACACTCGA GCCCACCGTA CTCGTC